

32. The polynucleotide of claim 27, wherein the polypeptide is cyclin A protein.

33. An isolated polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID: 6 have at least 80% identity based on the Clustal alignment method.

34. The polypeptide of claim 33, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 have at least 90% identity based on the Clustal alignment method.

35. The polypeptide of claim 33, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6 have at least 95% identity based on the Clustal alignment method.

36. The polypeptide of claim 33, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6.

37. The polypeptide of claim 33, wherein the polypeptide is a cyclin A protein.

38. A chimeric gene comprising the polynucleotide of claim 27 operably linked to a regulatory sequence.

39. An expression vector comprising the polynucleotide of claim 27.

40. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 27.

41. The cell produced by the method of claim 40.

42. An isolated polynucleotide comprising a nucleotide sequence comprised by the polynucleotide of claim 27, wherein the nucleotide sequence contains at least 30 nucleotides.

43. An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 80% identity based on the Clustal alignment method, or

(b) the complement of the nucleotide sequence.

44. The polynucleotide of claim 43, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 90% identity based on the Clustal alignment method.

45. The polynucleotide of claim 43, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 95% identity based on the Clustal alignment method.

46. The polynucleotide of claim 43 comprising the nucleotide sequence of SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, or SEQ ID NO: 15.

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47. The polynucleotide of claim 43, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16.

48. The polynucleotide of claim 43, wherein the polypeptide is a cyclin delta-1 protein.

49. An isolated polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 80% identity based on the Clustal alignment method.

50. The polypeptide of claim 49, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 90% identity based on the Clustal alignment method.

51. The polypeptide of claim 49, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16 have at least 95% identity based on the Clustal alignment method.

52. The polypeptide of claim 49, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16.

53. The polypeptide of claim 49, wherein the polypeptide is a cyclin delta-1 protein.

54. A chimeric gene comprising the polynucleotide of claim 43 operably linked to a regulatory sequence.

55. An expression vector comprising the polynucleotide of claim 43.

56. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 43.

57. The cell produced by the method of claim 56.

58. An isolated polynucleotide comprising a nucleotide sequence comprised by the polynucleotide of claim 43, wherein the nucleotide sequence contains at least 30 nucleotides.

59. An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 80% identity based on the Clustal alignment method, or

(b) the complement of the nucleotide sequence.

60. The polynucleotide of claim 59, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 90% identity based on the Clustal alignment method.

61. The polynucleotide of claim 59, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 95% identity based on the Clustal alignment method.

62. The polynucleotide of claim 59 comprising the nucleotide sequence of SEQ ID NO: 17, SEQ ID NO: 19, or SEQ ID NO: 21.

63. The polynucleotide of claim 59, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22.

64. The polynucleotide of claim 59, wherein the polypeptide is a cyclin delta-2 protein.

65. An isolated polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 80% identity based on the Clustal alignment method.

66. The polypeptide of claim 65, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 90% identity based on the Clustal alignment method.

67. The polypeptide of claim 65, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22 have at least 95% identity based on the Clustal alignment method.

68. The polypeptide of claim 65, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 18, SEQ ID NO: 20, or SEQ ID NO: 22.

69. The polypeptide of claim 65, wherein the polypeptide is a cyclin delta-2 protein.

70. A chimeric gene comprising the polynucleotide of claim 59 operably linked to a regulatory sequence.

71. An expression vector comprising the polynucleotide of claim 59.

72. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 59.

73. The cell produced by the method of claim 72.

74. An isolated polynucleotide comprising a nucleotide sequence comprised by the polynucleotide of claim 59, wherein the nucleotide sequence contains at least 30 nucleotides.

75. An isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 80% identity based on the Clustal alignment method, or

(b) the complement of the nucleotide sequence.

76. The polymucleotide of claim 75, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 90% identity based on the Clustal alignment method.

77. The polynucleotide of claim 75, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 95% identity based on the Clustal alignment method.

78. The polynucleotide of claim 75 comprising the nucleotide sequence of SEQ ID NO: 23, SEQ ID NO: 25, or SEQ ID NO: 27.

79. The polynucleotide of claim 75, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28.

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80. The polynucleotide of claim 75, wherein the polypeptide is a cyclin delta-3 protein.

81. An isolated polypeptide, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 80% identity based on the Clustal alignment method.

82. The polypeptide of claim 81, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 90% identity based on the Clustal alignment method.

83. The polypeptide of claim 81, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28 have at least 95% identity based on the Clustal alignment method.

84. The polypeptide of claim 81, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 24, SEQ ID NO: 26, or SEQ ID NO: 28.

85. The polypeptide of claim 81, wherein the polypeptide is a cyclin delta-3 protein.

86. A chimeric gene comprising the polynucleotide of claim 75 operably linked to a regulatory sequence.

87. An expression vector comprising the polynucleotide of claim 75.

88. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 75.

89. The cell produced by the method of claim 88.

90. An isolated polynucleotide comprising a nucleotide sequence comprised by the polynucleotide of claim 75, wherein the nucleotide sequence contains at least 30 nucleotides.

REMARKS

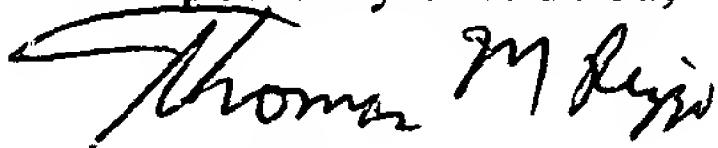
Claims 1-26 have been cancelled, and claims 27-90 have been added. Claims 27-90 are pending. It is respectfully requested that the amendments above be entered before examination of the application:

Support for sequence identities of 80%, 90%, and 95% is found on page 6, lines 32-37 of the specification. Support for claims 42, 58, 74, and 90 is found on page 7, line 14 of the specification.

Please charge a fee of \$1,102.00 to Deposit Account 04-1928  
(E. I. du Pont de Nemours and Company). If this fee is insufficient or incorrect, please charge or credit the balance to the above-identified account.

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,



THOMAS M. RIZZO  
ATTORNEY FOR APPLICANTS  
REGISTRATION NO. 41,272  
TELEPHONE: 302-892-7760  
FACSIMILE: 302-892-1026

Dated: November 9, 2000